

1636

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/424,951  
DATE: 03/05/2001  
TIME: 15:43:55

Input Set : A:\87714113.app  
Output Set: N:\CRF3\03052001\I424951.raw

ENTERED  
see p.5

3 <110> APPLICANT: SRIKANTHA, THYAGARAJAN  
4 SOLL, DAVID R.  
6 <120> TITLE OF INVENTION: CANDIDA ALBICANS TWO-COMPONENT HYBRID KINASE GENE,  
7 CANIK1, AND USE THEREOF  
9 <130> FILE REFERENCE: 087714/0113  
11 <140> CURRENT APPLICATION NUMBER: 09/424,951  
12 <141> CURRENT FILING DATE: 2000-01-20  
14 <150> PRIOR APPLICATION NUMBER: PCT/US98/11658  
15 <151> PRIOR FILING DATE: 1998-06-05  
17 <150> PRIOR APPLICATION NUMBER: 60/048,914  
18 <151> PRIOR FILING DATE: 1997-06-06  
20 <160> NUMBER OF SEQ ID NOS: 7  
22 <170> SOFTWARE: PatentIn Ver. 2.1  
24 <210> SEQ ID NO: 1  
25 <211> LENGTH: 1254  
26 <212> TYPE: DNA  
27 <213> ORGANISM: Candida albicans  
29 <220> FEATURE:  
30 <221> NAME/KEY: CDS  
31 <222> LOCATION: (1)..(1254)  
33 <400> SEQUENCE: 1  
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35 Glu Ile Arg Thr Pro Leu Asn Gly Ile Ile Gly Met Thr Gln Leu Ser  
36 1 5 10 15  
38 ctt gat aca gag ttg acr cag tac caa cga gag atg ttg tcg att gtg 96  
39 Leu Asp Thr Glu Leu Thr Gln Tyr Gln Arg Glu Met Leu Ser Ile Val  
40 20 25 30  
42 cat aac ttg gca aat tcc ttg ttg acc att ata gac gat ata ttg gat 144  
43 His Asn Leu Ala Asn Ser Leu Leu Thr Ile Ile Asp Asp Ile Leu Asp  
44 35 40 45  
46 att tct aag att gag gcg aat aga atg acg gtg gaa cag att gat ttt 192  
47 Ile Ser Lys Ile Glu Ala Asn Arg Met Thr Val Glu Gln Ile Asp Phe  
48 50 55 60  
50 tca tta aga ggg aca gtg ttt ggt gca ttg aaa acg tta gcc gtc aaa 240  
51 Ser Leu Arg Gly Thr Val Phe Gly Ala Leu Lys Thr Leu Ala Val Lys  
52 65 70 75 80  
54 gct att gaa aaa aac cta gac ttg acc tat caa tgt gat tca tcg ttt 288  
55 Ala Ile Glu Lys Asn Leu Asp Leu Thr Tyr Gln Cys Asp Ser Ser Phe  
56 85 90 95  
58 cca gat aat ctt att gga gat agt ttt aga tta cga caa gtt att ctt 336  
59 Pro Asp Asn Leu Ile Gly Asp Ser Phe Arg Leu Arg Gln Val Ile Leu  
60 100 105 110  
62 aac ttg gct ggt aat gct att aag ttt act aaa gag ggg aaa gtt agt 384  
63 Asn Leu Ala Gly Asn Ala Ile Lys Phe Thr Lys Glu Gly Lys Val Ser  
64 115 120 125  
66 gtt agt gtg aaa aag tct gat aaa atg gtg tta gat agt aag ttg ttg 432  
67 Val Ser Val Lys Lys Ser Asp Lys Met Val Leu Asp Ser Lys Leu Leu

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68	130	135	140	
70	tta gag gtt tgt gtt agc gac acg gga ata ggt ata gag aaa gac aaa	480		
71	Leu Glu Val Cys Val Ser Asp Thr Gly Ile Gly Ile Glu Lys Asp Lys			
72	145	150	155	160
74	ttg gga ttg att ttc gat acc ttc tgt caa gct gat ggt tct act aca	528		
75	Leu Gly Leu Ile Phe Asp Thr Phe Cys Gln Ala Asp Gly Ser Thr Thr			
76	165	170	175	
78	aga aag ttt ggt ggt aca ggt tta ggg ttg tca att tcc aaa cag ttg	576		
79	Arg Lys Phe Gly Thr Gly Leu Gly Leu Ser Ile Ser Lys Gln Leu			
80	180	185	190	
82	ata cat tta atg ggt gga gag ata ttg gtt act tcg gag tat gga tcc	624		
83	Ile His Leu Met Gly Gly Glu Ile Trp Val Thr Ser Glu Tyr Gly Ser			
84	195	200	205	
86	ggr tca aac ttt tat ttt acg gtg tgc gtg tcg cca tct aat att aga	672		
87	Gly Ser Asn Phe Tyr Phe Thr Val Cys Val Ser Pro Ser Asn Ile Arg			
88	210	215	220	
90	tat act cga caa acc gaa caa ttg tta cca ttt agt tcc cat tat gtg	720		
91	Tyr Thr Arg Gln Thr Glu Gln Leu Leu Pro Phe Ser Ser His Tyr Val			
92	225	230	235	240
94	tta ttt gta tcg act gag cat act caa gaa gaa ctt gat gtg ttg aga	768		
95	Leu Phe Val Ser Thr Glu His Thr Gln Glu Glu Leu Asp Val Leu Arg			
96	245	250	255	
98	gat gga att ata gaa ctt gga ttg ata cct ata ata gtg aga aat att	816		
99	Asp Gly Ile Ile Glu Leu Gly Leu Ile Pro Ile Ile Val Arg Asn Ile			
100	260	265	270	
102	gaa gat gca aca ttg act gag ccg gtg aaa tat gat ata att atg att	864		
103	Glu Asp Ala Thr Leu Thr Glu Pro Val Lys Tyr Asp Ile Ile Met Ile			
104	275	280	285	
106	gat tcg ata gag att gcc aaa aag ttg agg ttg tta tcg gag gtt aaa	912		
107	Asp Ser Ile Glu Ile Ala Lys Lys Leu Arg Leu Leu Ser Glu Val Lys			
108	290	295	300	
110	tat att ccg ttg gtt ttg gtc cat cat tct att cca cag ttg aat atg	960		
111	Tyr Ile Pro Leu Val Leu Val His His Ser Ile Pro Gln Leu Asn Met			
112	305	310	315	320
114	aga gta tgt att gat ttg ggg ata tct tcc tat gca aat acg cca tgt	1008		
115	Arg Val Cys Ile Asp Leu Gly Ile Ser Ser Tyr Ala Asn Thr Pro Cys			
116	325	330	335	
118	tcg atc acg gac ttg gcc agt gcg att ata cca gcg ttg gag tcg aga	1056		
119	Ser Ile Thr Asp Leu Ala Ser Ala Ile Ile Pro Ala Leu Glu Ser Arg			
120	340	345	350	
122	tct ata tca cag aac tca gac gag tcg gtg agg tac aaa ata tta cta	1104		
123	Ser Ile Ser Gln Asn Ser Asp Glu Ser Val Arg Tyr Lys Ile Leu Leu			
124	355	360	365	
126	gca gag gac aac ctc gtc aat cag aaa ctt gca gtt agg ata tta gaa	1152		
127	Ala Glu Asp Asn Leu Val Asn Gln Lys Leu Ala Val Arg Ile Leu Glu			
128	370	375	380	
130	aag caa ggg cat ctg gtg gaa gta gtt gag aac gga ctc gag gcg tac	1200		
131	Lys Gln Gly His Leu Val Glu Val Val Glu Asn Gly Leu Glu Ala Tyr			
132	385	390	395	400

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134 gaa gcg att aag agg aat aaa tat gat gtg gtg ttg atg gat gtg caa 1248
135 Glu Ala Ile Lys Arg Asn Lys Tyr Asp Val Val Leu Met Asp Val Gln
136      405      410      415
138 atg cct / 1254
139 Met Pro
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143 <211> LENGTH: 418
144 <212> TYPE: PRT
145 <213> ORGANISM: Candida albicans
147 <400> SEQUENCE: 2
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149 1 5 10 15
151 Leu Asp Thr Glu Leu Thr Gln Tyr Gln Arg Glu Met Leu Ser Ile Val
152 20 25 30
154 His Asn Leu Ala Asn Ser Leu Leu Thr Ile Ile Asp Asp Ile Leu Asp
155 35 40 45
157 Ile Ser Lys Ile Glu Ala Asn Arg Met Thr Val Glu Gln Ile Asp Phe
158 50 55 60
160 Ser Leu Arg Gly Thr Val Phe Gly Ala Leu Lys Thr Leu Ala Val Lys
161 65 70 75 80
163 Ala Ile Glu Lys Asn Leu Asp Leu Thr Tyr Gln Cys Asp Ser Ser Phe
164 85 90 95
166 Pro Asp Asn Leu Ile Gly Asp Ser Phe Arg Leu Arg Gln Val Ile Leu
167 100 105 110
169 Asn Leu Ala Gly Asn Ala Ile Lys Phe Thr Lys Glu Gly Lys Val Ser
170 115 120 125
172 Val Ser Val Lys Lys Ser Asp Lys Met Val Leu Asp Ser Lys Leu Leu
173 130 135 140
175 Leu Glu Val Cys Val Ser Asp Thr Gly Ile Gly Ile Glu Lys Asp Lys
176 145 150 155 160
178 Leu Gly Leu Ile Phe Asp Thr Phe Cys Gln Ala Asp Gly Ser Thr Thr
179 165 170 175
181 Arg Lys Phe Gly Gly Thr Gly Leu Gly Leu Ser Ile Ser Lys Gln Leu
182 180 185 190
184 Ile His Leu Met Gly Gly Glu Ile Trp Val Thr Ser Glu Tyr Gly Ser
185 195 200 205
187 Gly Ser Asn Phe Tyr Phe Thr Val Cys Val Ser Pro Ser Asn Ile Arg
188 210 215 220
190 Tyr Thr Arg Gln Thr Glu Gln Leu Leu Pro Phe Ser Ser His Tyr Val
191 225 230 235 240
193 Leu Phe Val Ser Thr Glu His Thr Gln Glu Leu Asp Val Leu Arg
194 245 250 255
196 Asp Gly Ile Ile Glu Leu Gly Leu Ile Pro Ile Ile Val Arg Asn Ile
197 260 265 270
199 Glu Asp Ala Thr Leu Thr Glu Pro Val Lys Tyr Asp Ile Ile Met Ile
200 275 280 285
202 Asp Ser Ile Glu Ile Ala Lys Lys Leu Arg Leu Leu Ser Glu Val Lys
203 290 295 300
205 Tyr Ile Pro Leu Val Leu Val His His Ser Ile Pro Gln Leu Asn Met

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PATENT APPLICATION: US/09/424,951

TIME: 15:43:55

Input Set : A:\87714113.app

Output Set: N:\CRF3\03052001\I424951.raw

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206 305          310          315          320
208 Arg Val Cys Ile Asp Leu Gly Ile Ser Ser Tyr Ala Asn Thr Pro Cys
209          325          330          335
211 Ser Ile Thr Asp Leu Ala Ser Ala Ile Ile Pro Ala Leu Glu Ser Arg
212          340          345          350
214 Ser Ile Ser Gln Asn Ser Asp Glu Ser Val Arg Tyr Lys Ile Leu Leu
215          355          360          365
217 Ala Glu Asp Asn Leu Val Asn Gln Lys Leu Ala Val Arg Ile Leu Glu
218          370          375          380
220 Lys Gln Gly His Leu Val Glu Val Val Glu Asn Gly Leu Glu Ala Tyr
221 385          390          395          400
223 Glu Ala Ile Lys Arg Asn Lys Tyr Asp Val Val Leu Met Asp Val Gln
224          405          410          415
226 Met Pro
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231 <211> LENGTH: 3246
232 <212> TYPE: DNA
233 <213> ORGANISM: Candida albicans
235 <220> FEATURE:
236 <221> NAME/KEY: CDS
237 <222> LOCATION: (1)..(3243) /
239 <400> SEQUENCE: 3
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241 Met Asn Pro Thr Lys Lys Pro Arg Leu Ser Pro Met Gln Pro Ser Val
242 1 5 10 15
244 ttt gaa ata ctc aac gac cct gag ctt tat agt cag cac tgt cat agc 96
245 Phe Glu Ile Leu Asn Asp Pro Glu Leu Tyr Ser Gln His Cys His Ser
246 20 25 30
248 ctt agg gaa aca ctt ctt gat cat ttc aac cat caa gct aca ctt atc 144
249 Leu Arg Glu Thr Leu Leu Asp His Phe Asn His Gln Ala Thr Leu Ile
250 35 40 45
252 gac act tat gaa cat gaa cta gaa aaa tcc aaa aat gcc aac aaa gcg 192
253 Asp Thr Tyr Glu His Glu Leu Glu Lys Ser Lys Asn Ala Asn Lys Ala
254 50 55 60
256 tcc caa caa gca ctt agt gaa ata ggt aca gtt gtt ata tct gtt gcc 240
257 Ser Gln Gln Ala Leu Ser Glu Ile Gly Thr Val Val Ile Ser Val Ala
258 65 70 75 80
260 atg gga gac ttg tcg aaa aaa gtt gag att cac aca gta gaa aat gac 288
261 Met Gly Asp Leu Ser Lys Lys Val Glu Ile His Thr Val Glu Asn Asp
262 85 90 95
264 cct gag att tta aaa gtc aaa atc acc atc aac acc atg atg gat caa 336
265 Pro Glu Ile Leu Lys Val Lys Ile Thr Ile Asn Thr Met Met Asp Gln
266 100 105 110
268 tta cag aca ttt gct aat gag gtt aca aaa gtc gcc acc gaa gtc gca 384
269 Leu Gln Thr Phe Ala Asn Glu Val Thr Lys Val Ala Thr Glu Val Ala
270 115 120 125
272 aat ggt gaa cta ggt gga caa gcg aaa aat gat gga tct gtt ggt att 432
273 Asn Gly Glu Leu Gly Gly Gln Ala Lys Asn Asp Gly Ser Val Gly Ile
274 130 135 140

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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/424,951

DATE: 03/05/2001  
TIME: 15:43:56

Input Set : A:\87714113.app  
Output Set: N:\CRF3\03052001\I424951.raw

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276 tgg aga tca ctt aca gac aat gtt aat att atg gct ctt aat tta act 480
277 Trp Arg Ser Leu Thr Asp Asn Val Asn Ile Met Ala Leu Asn Leu Thr
278 145 150 155 160
280 aac caa gtg cga gaa att gct gat gtc aca cgt gct gtt gcc aag ggg 528
281 Asn Gln Val Arg Glu Ile Ala Asp Val Thr Arg Ala Val Ala Lys Gly
282 165 170 175
284 gac ttg tca cgt aaa att aat gta cac gcc cag ggt gaa atc ctt caa 576
285 Asp Leu Ser Arg Lys Ile Asn Val His Ala Gln Gly Glu Ile Leu Gln
286 180 185 190
288 ctt caa cgt aca ata aac acc atg gtg gat cag tta cga acg ttt gca 624
289 Leu Gln Arg Thr Ile Asn Thr Met Val Asp Gln Leu Arg Thr Phe Ala
290 195 200 205
292 ttc gaa gta tct aaa gtt gct aga gat gtt ggt gtg ctt ggt ata tta 672
293 Phe Glu Val Ser Lys Val Ala Arg Asp Val Gly Val Leu Gly Ile Leu
294 210 215 220
296 gga gga caa gcg ttg att gaa aat gtt gaa ggt att tgg gaa gag ttg 720
297 Gly Gly Gln Ala Leu Ile Glu Asn Val Glu Gly Ile Trp Glu Glu Leu
298 225 230 235 240
300 act gat aat gtc aat gcc atg gct ctt aat ttg act aca caa gtg aga 768
301 Thr Asp Asn Val Asn Ala Met Ala Leu Asn Leu Thr Thr Gln Val Arg
302 245 250 255
304 aat att gcc aat gtc acc act gcc gtt gcc aag ggt gat ttg tcg aaa 816
305 Asn Ile Ala Asn Val Thr Thr Ala Val Ala Lys Gly Asp Leu Ser Lys
306 260 265 270
308 aaa gtc act gct gat tgt aag gga gaa aty ctt gat ttg aaa ctt act 864
309 Lys Val Thr Ala Asp Cys Lys Gly Glu Ile Leu Asp Leu Lys Leu Thr
310 275 280 285
312 att aat caa atg gtg gac cga tta cag aat ttt gct ctt gcg gtg acg 912
313 Ile Asn Gln Met Val Asp Arg Leu Gln Asn Phe Ala Leu Ala Val Thr
314 290 295 300
316 aca ttg tcg aga gag gtt ggt act ttg ggt att ttg ggt gga caa gct 960
317 Thr Leu Ser Arg Glu Val Gly Thr Leu Gly Ile Leu Gly Gly Gln Ala
318 305 310 315 320
320 aac gta cag gat gtt gaa ggt gct tgg aaa cag gtt aca gaa aat gtc 1008
321 Asn Val Gln Asp Val Glu Gly Ala Trp Lys Gln Val Thr Glu Asn Val
322 325 330 335
324 aac cta atg gct act aat tta act aac caa gtg aga tct att gct aca 1056
325 Asn Leu Met Ala Thr Asn Leu Thr Asn Gln Val Arg Ser Ile Ala Thr
326 340 345 350
328 gtt act act gca gtt gcg cat ggt gat ttg tcg caa aag att gat ggt 1104
329 Val Thr Thr Ala Val Ala His Gly Asp Leu Ser Gln Lys Ile Asp Gly
330 355 360 365
332 cat ccc aaa gga gag att tta caa ttg aaa aat aca atc aac aag atg 1152
333 His Pro Lys Gly Glu Ile Leu Gln Leu Lys Asn Thr Ile Asn Lys Met
334 370 375 380
336 gtg gac tct ttg cag ttg ttt gca tca gaa gtg tcg aaa gtg gca caa 1200
337 Val Asp Ser Leu Gln Leu Phe Ala Ser Glu Val Ser Lys Val Ala Gln
338 385 390 395 400
340 gat gtt ggt att aat gga aaa tta ggt att caa gca caa gtt agt gat 1248

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**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/424,951

DATE: 03/05/2001

TIME: 15:43:57

Input Set : A:\87714113.app

Output Set: N:\CRF3\03052001\I424951.raw

L:743 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5

L:760 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:777 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

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